

60  
 1 ATGTGGAAATGGATACTGACACATTGTGCCTCAGCCTTTCCCCACCTGCCCCGGCTGTCTGC  
 -----+-----+-----+-----+-----+-----+-----+  
 TACACCTTTACCTATGACTGTGTAACACGGAGTCGGAAGGGGTGGACGGGCCGACGACG  
 -----+-----+-----+-----+-----+-----+-----+  
M W K W I L L T H C A S A F P H L P G C C C  
 61 TGCTGCTGCTTTTGTGTGTTCTTGGTGCTTCCGTCCTGTCACCTGCCAAGCCCTT  
 -----+-----+-----+-----+-----+-----+-----+  
 ACGACGACGAAAAACAACGACAAGAACCACAGAAGGCAGGGACAGTGGACGGTTCGGGAA  
 -----+-----+-----+-----+-----+-----+-----+  
C C C F L L L F L V S S V P V I C Q A L  
 121 GGTCAAGGACATGGTGTCAACGAGGCCACCAACTCTTCTCCCTCCTCTCCTCTCCT  
 -----+-----+-----+-----+-----+-----+-----+  
 CCAGTCCTGTACCCACAGTGGTCTCCGGTGTGAGAAAGAGGAGGAGGAGGAGGAGGA  
 -----+-----+-----+-----+-----+-----+-----+  
 G Q D M V S P E A T N S S S S S S S P  
 181 TCCAGCGCGGGAAGGCATGTGCGGAGCTACAATCACCTTCAAGGAGATGTCGCGTGGAGA  
 -----+-----+-----+-----+-----+-----+-----+  
 AGGTCGCGCCCTTCCGTACACGCCTCGATGTTAGTGAAGTTCCTCTACAGGCGACCTCT  
 -----+-----+-----+-----+-----+-----+-----+  
 S S A G R H V R S Y N H L Q G D V R W R

FIG. 1A

MATCH WITH FIG.1A

241 AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGTCAAGCGGG  
 -----+-----+-----+-----+-----+-----+-----+  
 TTCGATAAGAGAAAGTGGTTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC 300

K L F S F T K Y F L K I E K N G K V S G

301 ACCAAGAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAAATCGGAGTT  
 -----+-----+-----+-----+-----+-----+-----+  
 TGGTTCTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA 360

T K K E N C P Y S I L E I T S V E I G V

361 GTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAAGGGAAACTC  
 -----+-----+-----+-----+-----+-----+-----+  
 CAACGGCAGTTTCGGTAAATTGTCGTTGATAATGAATCGGTACTTGTCTTCCCTTTGAG 420

V A V K A I N S N Y Y L A M N K K K L

421 TATGGCTCAAAAGAAATTTAAACAATGACTGTAGCTGAAGGAGAGGATAGAGGAAAAATGGA  
 -----+-----+-----+-----+-----+-----+-----+  
 ATACCGAGTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT 480

Y G S K E F N N D C K L K E R I E E N G

MATCH WITH FIG.1C

FIG.1B

MATCH WITH FIG. 1B

481	TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG	540
	-----+-----+-----+-----+-----+-----+-----+	
	ATGTTATGGATAGTAGTAAATTGACCGTCGTATTACCCCTCCGTTTACATACACCCGTAAC	
	Y N T Y A S F N W Q H N G R Q M Y V A L	
541	AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAAACACGAAAGGAAAAACACCTCTGCTCAC	600
	-----+-----+-----+-----+-----+-----+-----+	
	TTACCTTTTCCTCGAGGTTCCCTCCTCCTCTTTTGTGCTTCCCTTTTGTGGAGACGAGTG	
	N G K G A P R R G Q K T R R K N T S A H	
601	TTTCTTCCAATGGGTACACTCATAG	627
	-----+-----+-----	
	AAAGAAGGTTACCACCATGTGAGTATC	
	F L P M V V H S *	

FIG.1C

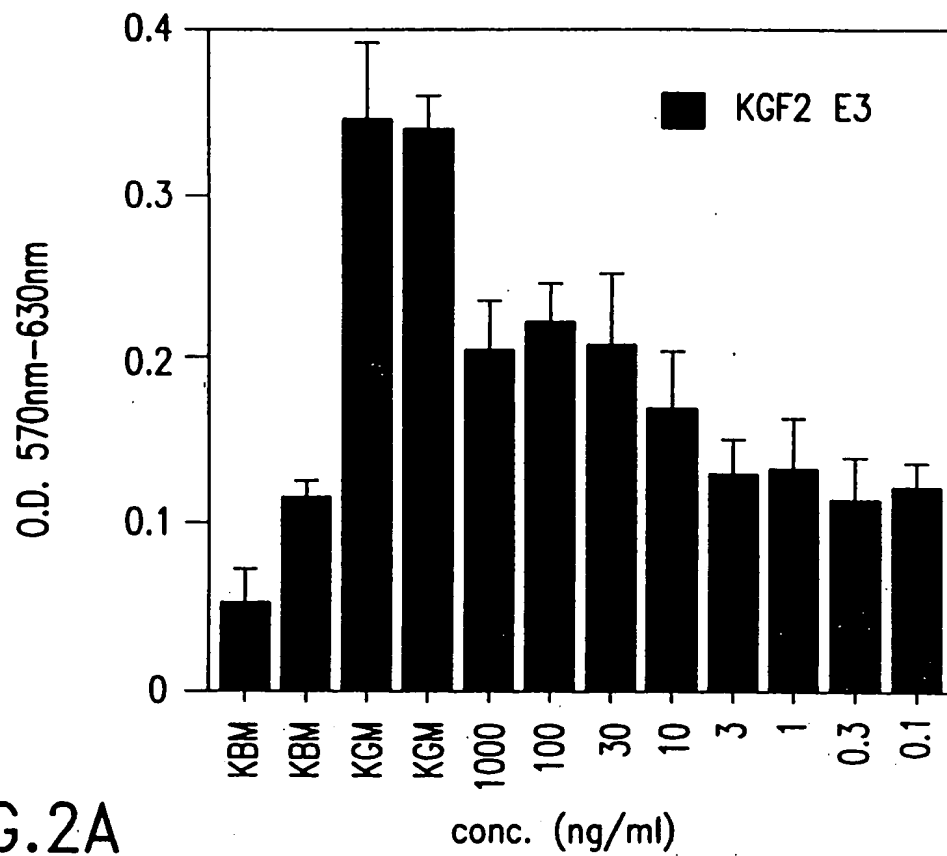


FIG.2A

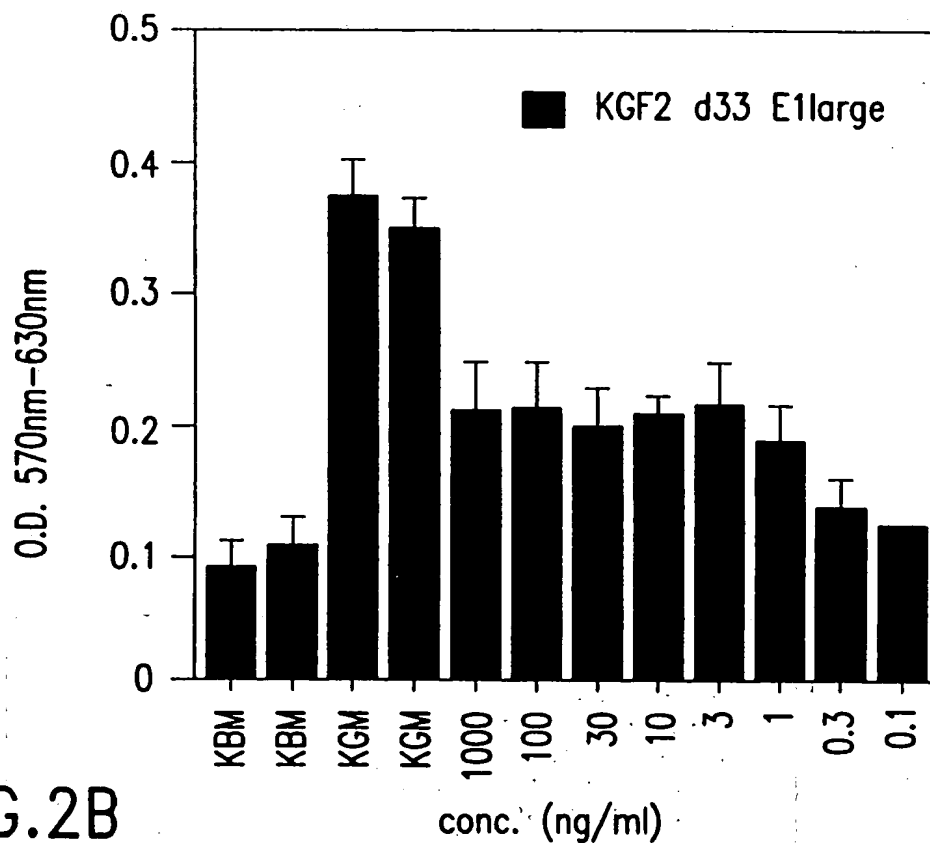


FIG.2B

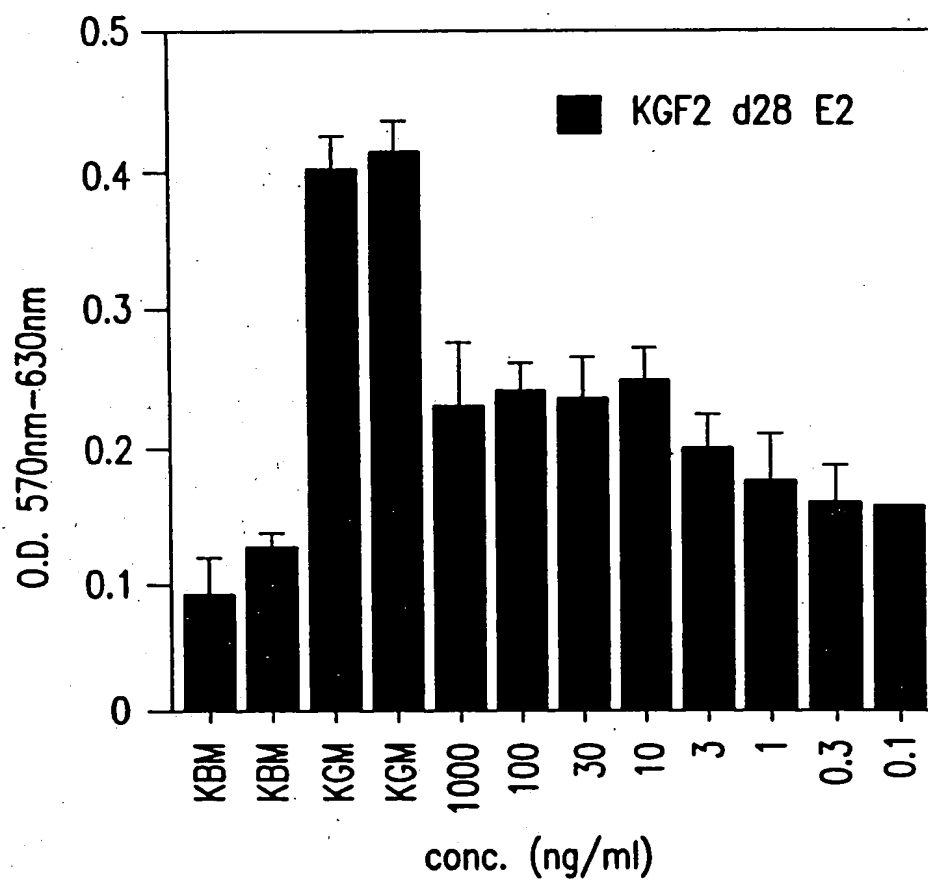


FIG.2C

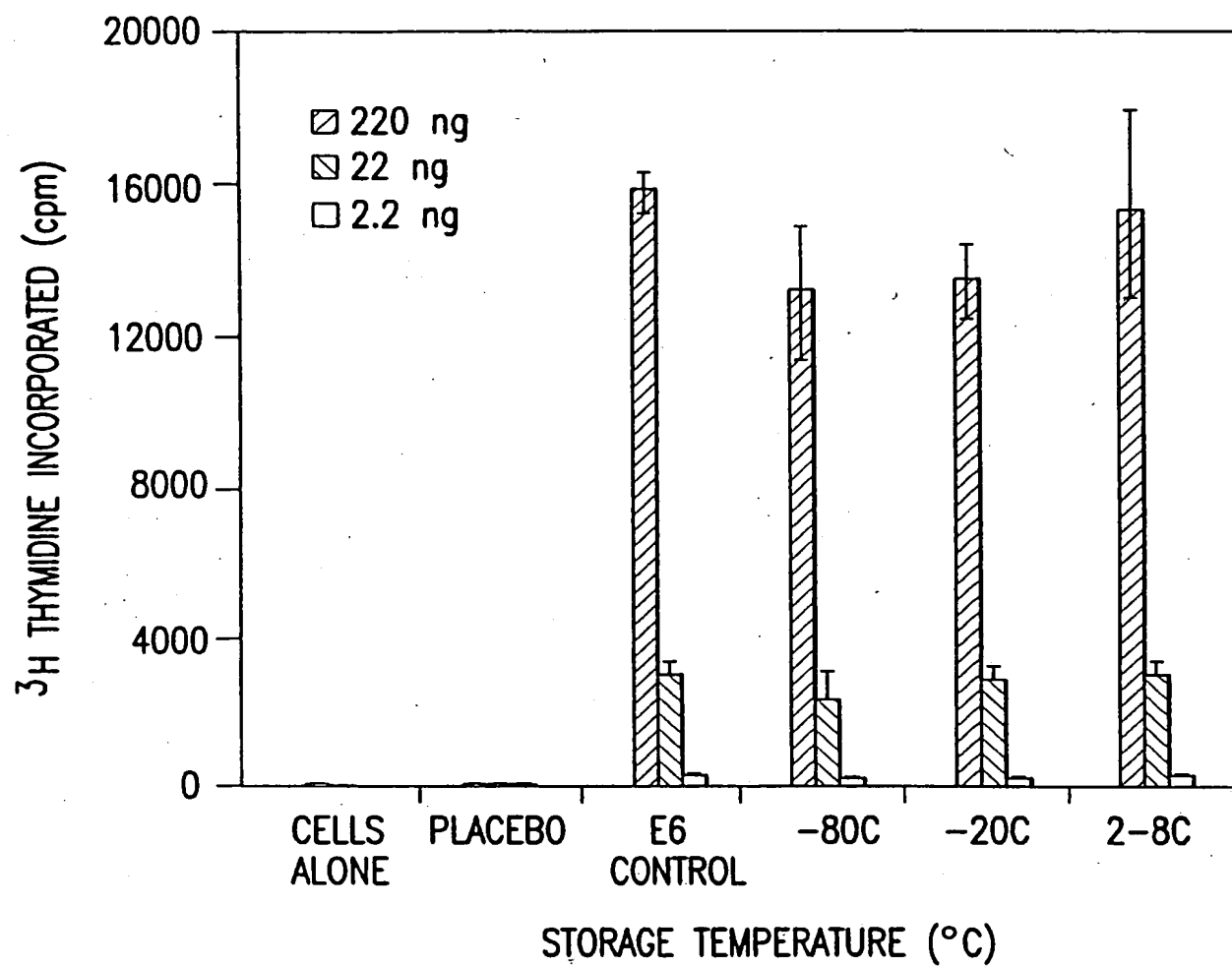


FIG.3

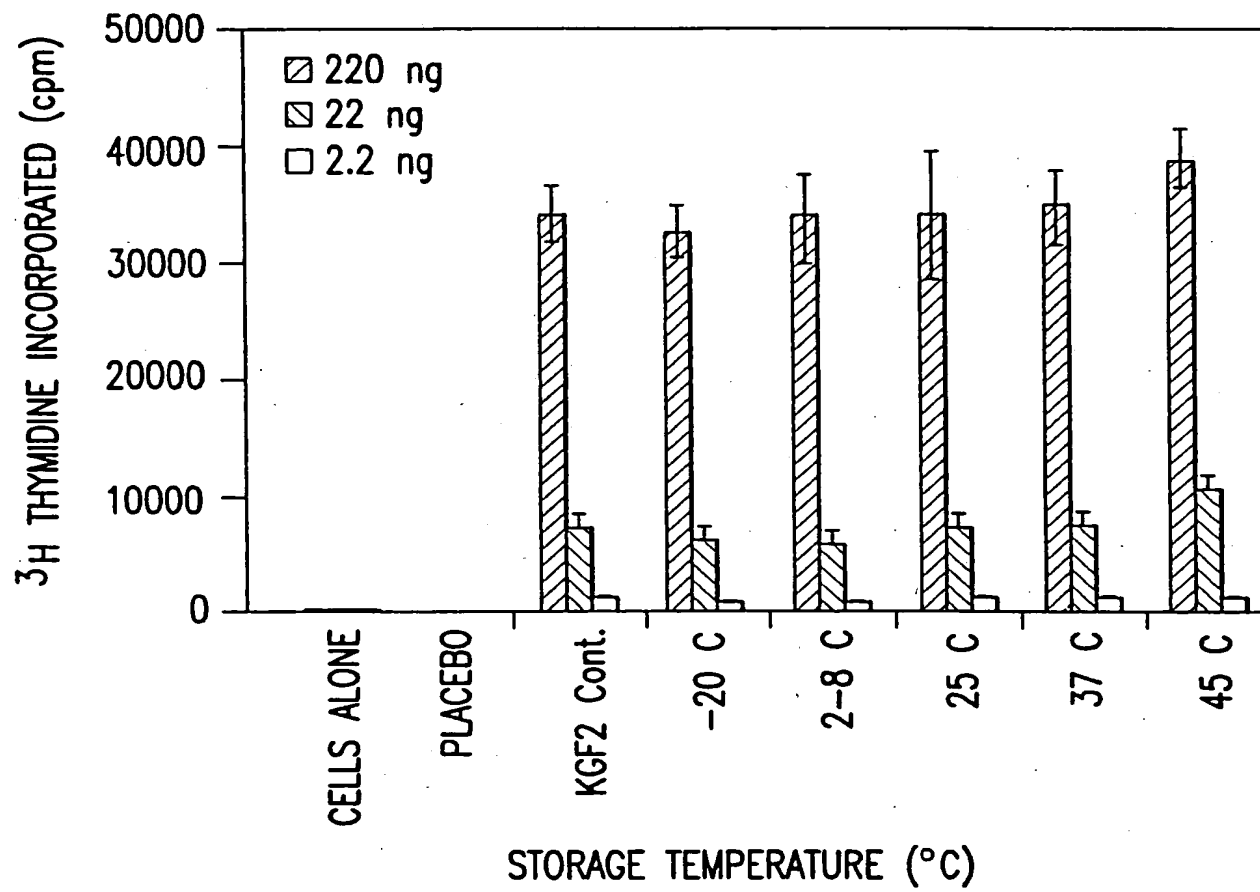


FIG.4

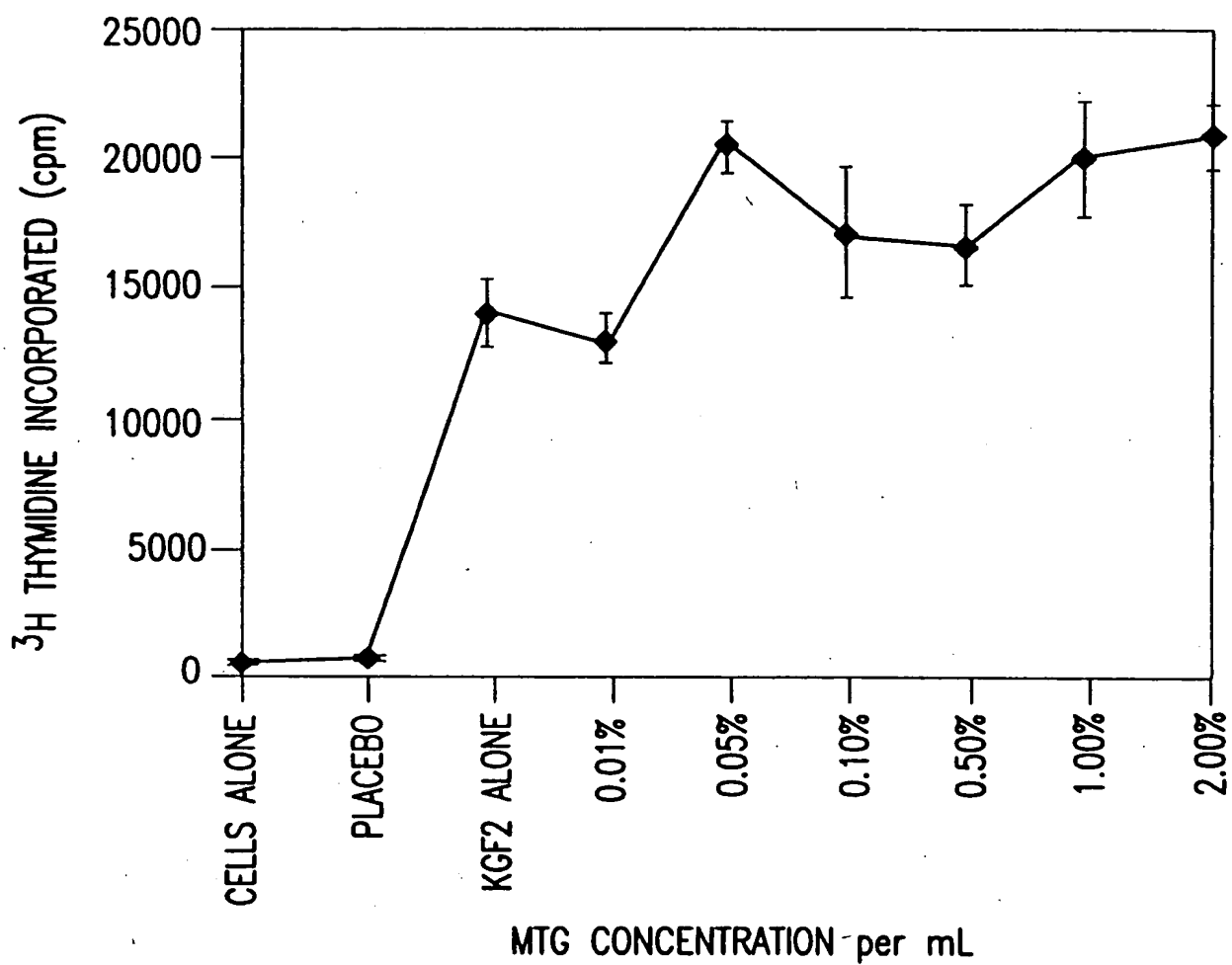


FIG.5